Fig. 10

human   : GDVEKGKKIFIMKCSQCHTVEGGKHKTGPNLHGLFGRK   SEQ ID NO: 1
bacterium : EGDAAAGEKVSKKCLACHTFDQGGANKVGPNPNLFGVF   SEQ ID NO: 2

LCS   : GDlx3.3IGlx0.1IKlx0.2IKlx4.0IKClx2.2ICHTlx3.3IGGlx2.2IK
           GDlx1.4IElx0.2IKlx0.2IKlx0.4IKClx2.2ICHTlx3.3IGGlx2.2IK

homology : 47%

Fig. 11

Rat : MSLAILRVIRLVRVFRIFKLSRHSKGLQILGRTLKASMRELGLLIFFIGVV

leucnzip. L I6I L I6I L I6I L I6I L
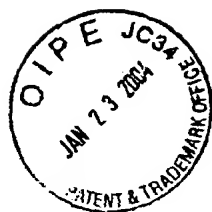
SEQ ID NO: 3

Fig. 12

human   : GDVEK G K KIFIMKCSQCHTVEKGG KHKTGPNLHGLFGRK...   SEQ ID NO: 1
bacterium: E GDAAAGEKVSK KCLACHTFDQGGANKV GPNPN LFGVF...   SEQ ID NO: 2
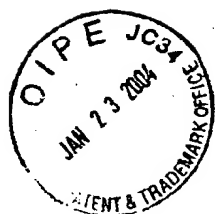
Fig. 23 A

```
  1  T E E Q I A E F K E    A F S L F D K D G D
 21  G T I T T K E L G T    V M R S L G Q N P T
 41  E A E L Q D M I N E    V D A D G N G T I D
 61  F P E F L T M M A R    K M K D T D S E E E
 81  I R E A F R V F D K    D G N G Y I S A A E
101  L R H V M T N L G E    K L T D E E V D E M
121  I R E A N I D G D G    Q V N Y E E F V Q M
141  M T A
```

AMINO ACID SEQUENCE OF CALMODULIN   SEQ ID NO: 4
(EXCERPT FROM PDB)

Fig. 23 B

```
  1  A M D Q Q A E A R A    F L S E E M I A E F
 21  K A A F D M F D A D    G G G D I S T K E L
 41  G T V M R M L G Q N    P T K E E L D A I I
 61  E E V D E D G S G T    I D F E E F L V M
 81  V R Q M K E D A K G    K S E E E L A D C F
101  R I F D K N A D G F    I D I E E L G E I L
121  R A T G E H V T E E    D I E D L M K D S D
141  K N N D G R I D F D    E F L K M M E G V Q
161
```

AMINO ACID SEQUENCE OF TROPONIN C   SEQ ID NO: 5
(EXCERPT FROM PDB)

Fig. 25

Probe site = 81-108 In Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	SEQ ID NO: 6 < target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe > SEQ ID NO: 7

111	112	113	114	115	116	117	118	119	120	121	122	123	
I	D	I	E	E	L	G	E	I	R	A	T		SEQ ID NO: 6 < target >
S	A	A	E	L	R	H	V	M	T	N	L		< probe > SEQ ID NO: 7

rmsd = 0.567034

Fig. 26

Probe site = 81-108 and 117-143 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	SEQ ID NO: 6 < target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe > SEQ ID NO: 7

111	112	113	114	115	116	117	118	119	120	121	122	123	
I	D	I	E	E	L	G	E	I	L	R	A	T	< target I >SEQ ID NO: 6
I	S	A	A	E	L	R	H	V	M	T	N	L	< probe >SEQ ID NO: 7

132	133	134	135	136	137	138	139	140	141	142	143	144	145	
I	E	D	L	M	K	D	S	D	K	N	N	D	G	SEQ ID NO: 8 < target >
V	D	E	M	I	R	E	A	N	I	D	G	D	G	< probe > SEQ ID NO: 9

146	147	148	149	150	151	152	153	154	155	156	157	158	
R	I	D	F	D	E	F	L	K	M	M	E	G	< target >SEQ ID NO: 8
Q	V	N	Y	E	E	F	V	Q	M	M	T	A	< probe >SEQ ID NO: 9

rmsd = 0.823665

Fig. 29


```
================ ATP/GTP binding site ====================

Probe = (elongation factor)

7 8 9 10 11 12 13 14
G H V D H G K T   < probe >        SEQ ID NO: 10

-----

8 9 10 11 12 13 14 15
G A P G S G K G   < target >       SEQ ID NO: 11
G H V D H G K T   < probe >        SEQ ID NO: 10
rmsd=0.648732  adenylate kinase

unit - A

   ...   ...   ...

10 11 12 13 14 15 16 17
G A G G V G K S   < target >       SEQ ID NO: 12
G H V D H G K T   < probe >        SEQ ID NO: 10
rmsd=0.421770  ras protein
```
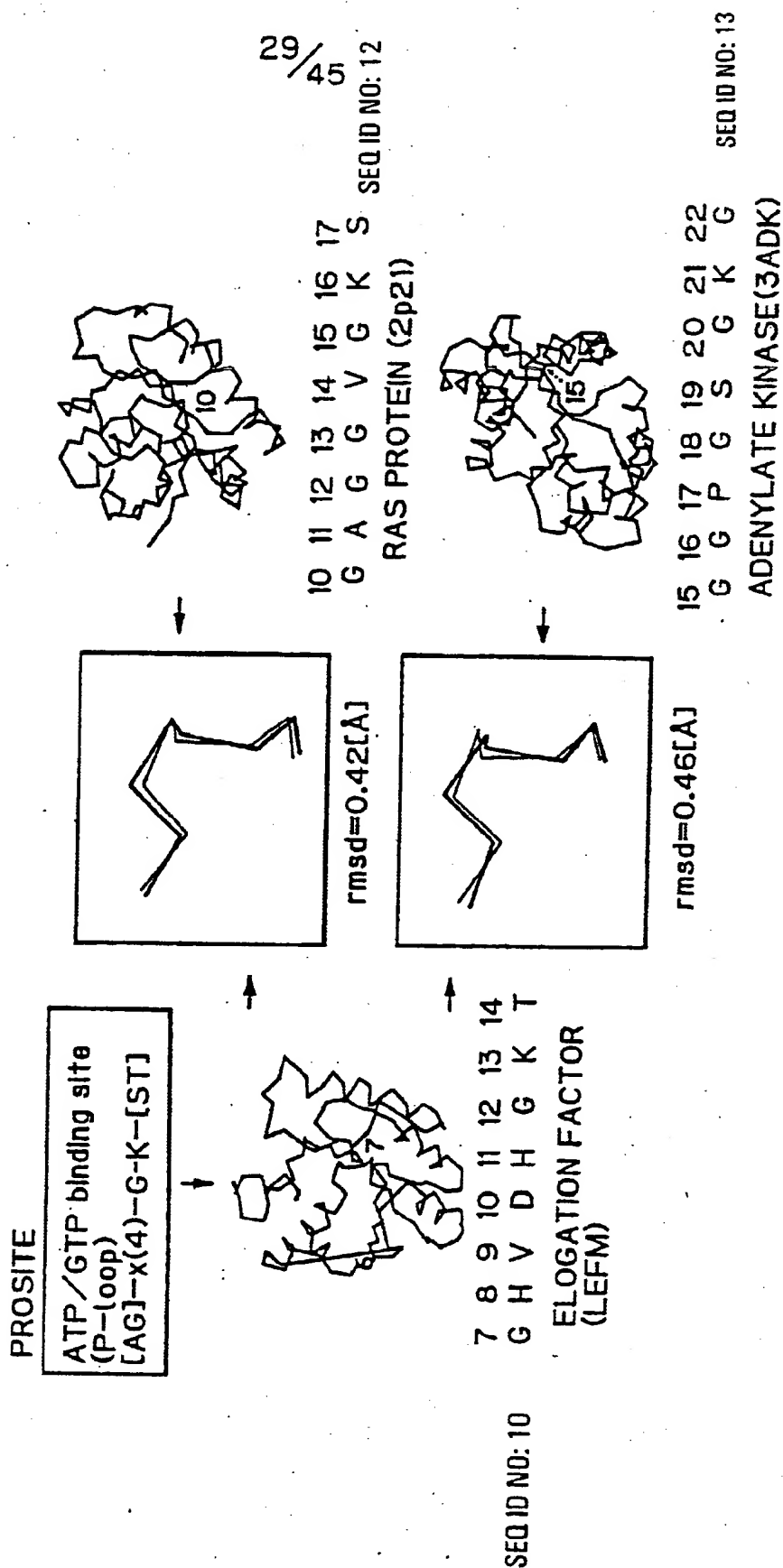
Fig. 30

PROSITE

ATP/GTP binding site
(P-loop)
[AG]-x(4)-G-K-[ST]

SEQ ID NO: 10

7 8 9 10 11 12 13 14
G H V D H G K T
ELOGATION FACTOR
(LEFM)

rmsd=0.42[Å]

rmsd=0.46[Å]

10 11 12 13 14 15 16 17
G A G G V G K S   SEQ ID NO: 12
RAS PROTEIN (2p21)

15 16 17 18 19 20 21 22
G G P G S G K G   SEQ ID NO: 13
ADENYLATE KINASE(3ADK)

Fig. 38 A

```
    1   I V G G Y T C C A N     T V P Y Q V S L N S
   21   G Y H F C G G S L I     N S Q W V V S A A H
   41   C Y K S G I Q V R L     G E D N I N V V E G
   61   N E Q F I S A S K S     I V H P S Y N S N T
   81   L N N D I M L I K L     K S A A S L N S R V
  101   A S I S L P T S C A     S A G T Q C L I S G
  121   W G N T K S S G T S     Y P D V L K C L K A
  141   P I L S D S S C K S     A Y P G Q I T S N M
  161   F C A G Y L E G G K     D S C Q G D S G G P
  181   V V C S G K L Q G I     V S W G S G C A Q K
  201   N K P G V Y T K V C     N Y V S W I K Q T I
  221   A S N              SEQ ID NO: 14
```

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

Fig. 38 B

```
    1   V V G G T E A Q R N     S W P S Q I S L Q Y
   21   R S G S S W A H T C     G G T L I R Q N W V
   41   M T A A H C V D R E     L T F R V V V G E H
   61   N L N Q N N G T E Q     Y V G V Q K I V V
   81   P Y W N T D D V A A     G Y D I A L L R L A
  101   Q S V T L N S Y V Q     L G V L P R A G T I
  121   L A N S P C Y I T T     G W G L T R T N G Q
  141   L A Q T L Q Q A Y L     P T V D Y A I C S S
  161   S S Y W G S T V K N     S M V C A G G D G V
  181   R S G C Q G D S G G     P L H C L V N G Q Y
  201   A V H G V T S F V S     R L G C N V T R K P
  221   T V F T R V S A Y I     S W I N N V I A S N
                         SEQ ID NO: 15
```

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

Fig. 39 A

```
Key site number 36 — 41 in Trypsin

41 42 43 44 45 46
 M  T  A  A  H  C    ⟨ target ⟩ SEQ ID NO: 16
 V  S  A  A  H  C    ⟨ probe ⟩ SEQ ID NO: 17

d = 12.070038 [A]
r.m.s.d. = 0.061077 [A]
The number of atoms in a probe = 6
The number of atoms in PDB = 240
The number of combination = 1
Time = 1sec
```

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

Fig. 39 B

```
Key site number 175 — 179 in Trypsin

186 187 188 189 190
  G   D   S   G   G    ⟨ target ⟩ SEQ ID NO: 18
  G   D   S   G   G    ⟨ probe ⟩ SEQ ID NO: 19

d = 8.922721 [A]
r.m.s.d. = 0.092879 [A]
The number of atoms in a probe = 5
The number of atoms in PDB = 240
The number of combination = 1
Time = 1sec
```
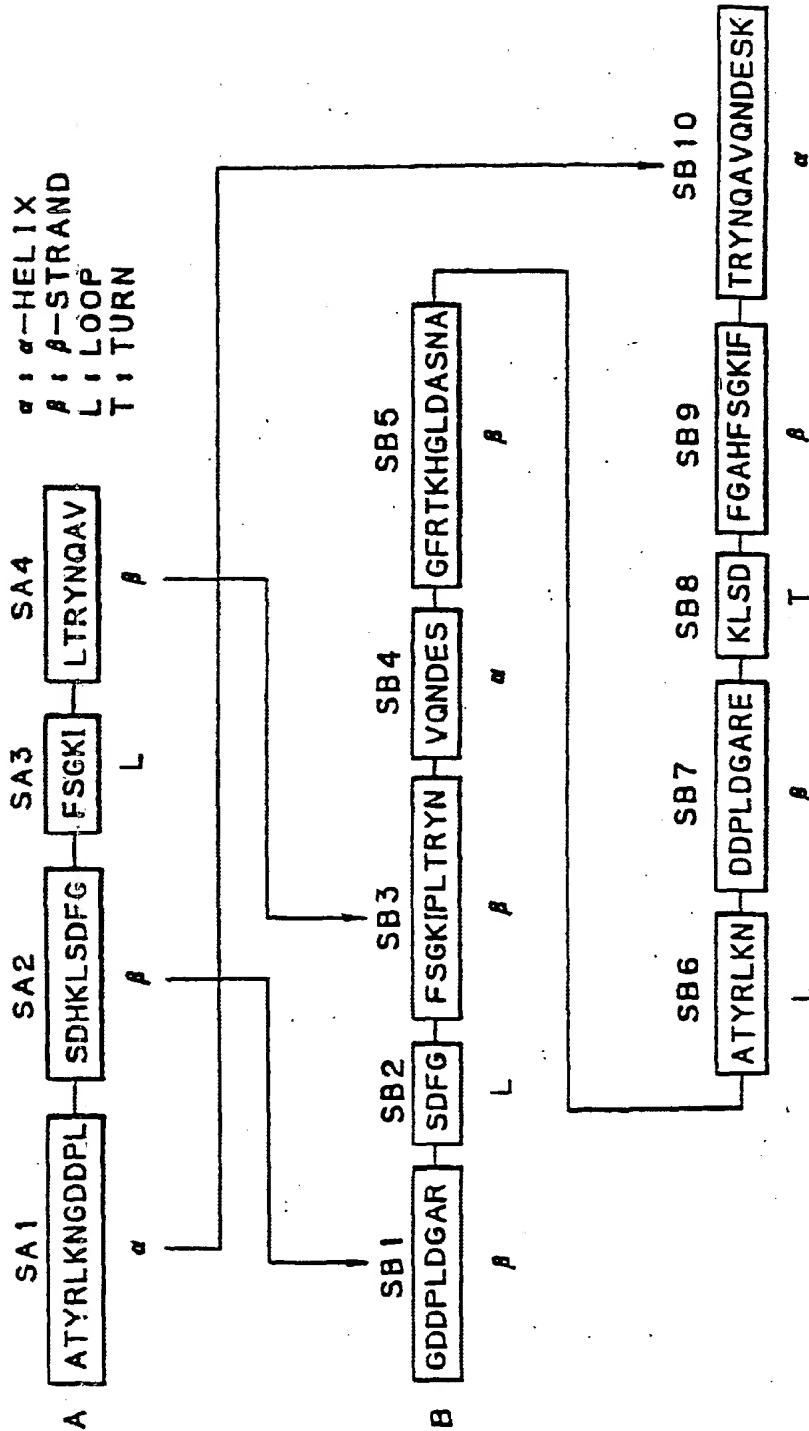
RETRIEVED RESULTS OF SERINE ACTIVE SITES

Fig. 46

α : α-HELIX
β : β-STRAND
L : LOOP
T : TURN

A

SA1	SA2	SA3	SA4
ATYRLKNGDDPL	SDHKLSDFG	FSGKI	LTRYNQAV
α	β	L	β

B

SB1	SB2	SB3	SB4	SB5
GDDPLDGAR	SDFG	FSGKIPLTRYN	VQNDES	GFRTKHGLDASNA
β	L	β	α	β

SB6	SB7	SB8	SB9	SB10
ATYRLKN	DDPLDGARE	KLSD	FGAHFSGKIF	TRYNQAVQNDESK
L	β	T	β	α

SEQ ID NO: 20